

Arabidopsis (provided as SEQ ID NO:1, 2, 3 and 4, respectively), using the conventional single letter representations for the amino acids. Capital letters indicate identity to the barley sequence. This sequence comparison information can be combined with information about predicted secondary structure of the protein, available from computer analysis of the sequence, to begin to identify sites for mutation to create better thermostability.--

Please replace paragraph 00031 on page 9 of the application with the following:

--[00031] Mutagenesis. Mutagenesis was done using the Muta-Gene kit (BIO-RAD). Barley α -glucosidase cDNA was sub-cloned into the EcoRI site of the phagemid pTZ18U (BIO-RAD, Hercules, CA). E. coli strain CJ236 (Kunkel et al., 1987) was used to generate dU-substituted DNA and single stranded DNA was isolated using the helper phage M13K07 (BIO-RAD). For the mutant R336P, the oligonucleotide CGGTGAAGTTGACAGGATCCAAGGTGAAG (SEQ ID NO:5) (5', reverse complement) was used to replace the codon for arginine (CGT) with a codon for proline (CCT) and to remove a Tth111I site. For the mutant T340P, the oligonucleotide GAGCTCGGCGGCGGGGAAGTTTACACGGTC (SEQ ID NO:6) was used to replace the codon for threonine (ACC) with a codon for proline (CCC) and to remove a Tth111I site. For the mutant A742P, the oligonucleotide CCAGGAGGTGGAACGGGGTCCGGCGC (SEQ ID NO:7) was used to replace the codon for alanine (GCG) with a codon for proline (CCG) and to remove a RsrII site.--

In the drawings:

Per 37 C.F.R. 1.121(d), the applicants submit the enclosed Fig. 2 with the proposed changes shown in red for approval by the Examiner.